REMARKS

1. Applicants hereby submit the following:
a paper copy of a "Sequence Listing", complying with §1.821(c), to be incorporated into the specification as directed above;
the Sequence Listing in computer readable form, complying with §1.821(e) and §1.824, including, if an amendment to the paper copy is submitted, all previously submitted data with the amendment incorporated therein.

1.1. According to the office action, applicants have not yet filed a paper copy of the Sequence Listing. According to our transmittal letter of October 14, 2004, a paper copy was filed. A copy of our postcard receipt is enclosed.

Since we agree that a CRF is needed, we nonetheless enclose a courtesy copy of the paper copy, too.

1.3. Claims 1 and 134-138 recite amino acid sequences with fewer than four specifically identified amino acids and hence are outside the scope of 37 CFR 1.821(a). If these sequences were set forth in the sequence listing, it would be as

Pro-Xaa-Xaa-Xaa-Pro,

in which the two Pro were the only specifically identified amino acids.

1.3. Claims 73 and 74 have been amended to reference SEQ ID NO:2.

2. The description is believed to be in compliance with §1.821(d).

3. The undersigned attorney or agent hereby states as follows:

(a) this submission does not include new matter [§1.821(g)];

(b) the contents of the paper copy (as amended, if applicable) and the computer readable form of the Sequence Listing, are the same [§1.821(f) and §1.825(b)];

(c) if the paper copy has been amended, the amendment is supported by the specification and does not include new matter [§1.825(a)]; and

(d) if the computer readable form submitted herewith is a substitute for a form found upon receipt by the PTO to be damaged or unreadable, that the substitute data is identical to that originally filed [§1.825(d)].

4. Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs

in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Respectfully submitted,

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